In the specification:

On page 4 and 5 of the specification please replace the bridging paragraph between these two pages with the following paragraph:

Endothelial cells lining blood vessels express organ-specific markers and this heterogeneity at the molecular level of the vascular system can potentially be used for the specific binding of chemotherapeutic agents. Endothelial cells in angiogenic vessels express their own set of integrin and aminopeptidase-N cell-surface receptors, which differ from the non-angiogenic set of markers. Integrins, which are heterodimers composed of α and β subunits (e.g. $\alpha_v\beta_3$, $\alpha_v\beta_5$) are known to mediate cell adhesion and are involved in cell migration. Aminopeptidase-N (APN) is a 140-kDa protein, which has been associated with cell migration and tumor invasion. These molecular addresses are known to recognize and internalize short amino acid sequences into the cells. During the last decade, phage display libraries have been used to select in vivo for peptides recognized by the vascular endothelium of normal tissues and malignant tumors. Recovery of the phage form the tumors led to the identification of two peptide sequences CNGRCVSGCAGRC (SEQ ID NO: 1) and CDCRGDCFC (SEQ ID NO: 2). The three-amino acids peptide sequences Asn-Gly-Arg (NGR) and Arg-Gly-Asp (RGD), either containing cysteins or not, were found to interact specifically with integrins, APN receptors and additionally internalized into tumor cells. Phage containing these peptides homed to human breast carcinoma, human Kaposi's sarcoma and mouse melanoma. Additionally these peptide sequences were successfully used as a vehicle to selectively delivering in vivo and in vitro a pro-apoptotic peptide and the anticancer drug doxorubicin.

On page 18 of the specification, please replace the last line with the following line:

Figure 7 depicts an HPLC chromatograph for purified NGR-NH_2.

On page 19 of the specification, please replace the first 9 lines with the following lines:

Figure 8 depicts an HPLC chromatograph for purified RGD-NH_2.

Figure 9 depicts a mass spectrum for purified NGR-NH_2.

Figure 10 depicts a mass spectrum for purified NGD-NH_2.

Figure 11 depicts an ^{1}H NMR spectrum in D_2O of a collected HPLC peak for NGR-NH_2.

Figure 12 depicts depicts an ^{1}H NMR spectrum in D_2O of a collected HPLC peak for NGR-NH_2.

Figure 13 depicts the ^{13}C-NMR spectrum for the HPLC peak collected at 6.4 minutes for NGR-NH_2 showing some impurities at ~163 and 117 ppm.

On page 58 of the specification, please replace the last paragraph with the following paragraph:

Non-limiting examples of targeting moieties suitable for the subject coordination complexes of the present invention include peptides. The syntheses of the peptide sequences NGR-NH_2, NH_2CNGRC-GG (SEQ ID NO: 3) and RGD-NH_2 were performed by using an Advanced Chemtec batch peptide synthesizer. Scheme 3 depicts the automated steps taken for the synthesis of NGR-NH_2 but the same is applicable for the synthesis of any peptide sequence. A Rink amide resin was used as the solid support, which incorporates an NH_2 moiety to the C-terminus of the first loaded amino acid when the peptide is cleaved out of the resin, thus the obtained peptides contain an amide-capped C-terminus. The overall synthesis consists of coupling each the amino acids to either the Fmoc-deprotected resin or another amino acid by DIC/HOBt. In each case this is followed by the cleavage of the Fmoc on the coupled amino acid by piperidine (20%)/DMF.

On page 59 of the specification, please replace lines 2-3 with the following lines:

Scheme 3. Solid phase NGR-NH_2 synthesis. Automated synthetic steps: (1) DIC/HOBt, DMF, (2) 20% piperidine.

On page 59 of the specification, please replace Table 1 with the following Table 1:

Table 1.

Peptide	m/z observed	m/z calculated
NGR-NH_2	345.89	345.37
NH_2CNGRC-GG (SEQ ID NO: 3)	665.13	665.77
RGD-NH_2	346.94	346.36

On page 59 of the specification, please replace the second full paragraph with the following paragraph:

The purification of the NGR-NH_2 and RGD-NH_2 peptides by C18-HPLC was successful. For each peptide two peaks were collected from the HPLC (Figures 7 and 8) which corresponded to products with the desired mass (Figure 9 and 10). For NGR-NH_2, the collected peaks had retention times of 4.8 and 6.4 minutes and for RGD-NH_2, 4.8 and 5.6 minutes.

On pages 59 and 60 of the specification, please replace the bridging paragraph between these two pages with the following paragraph:

The ^{1}H- and ^{13}C-NMR spectra in D_2O of both collected peaks for NGR-NH_2 were recorded in order to see if they correspond to the same isomer. The only difference in the ^{1}H-NMR spectrum was the signal corresponding to the C_β-H of Asn, which only for the peak collected at 6.4 minutes was resolved as two sets of doublets (Figure 11 and 12).

On page 60 of the specification, please replace the first full paragraph with the following paragraph:

Additionally, the ^{13}C-NMR spectrum for the peak collected at 6.4 minutes showed some impurities at ~163 and 117 ppm which appear slightly in the peak collected at 5.6 minutes (Figure 13). Based on these results one possible explanation may be that the detected impurities may become trapped in the peptide leading to a partial folding. NMR studies for the peptide RGD-NH_2 were not pursued but it is believed to behave similarly.

On pages 60 and 61 of the specification, please replace bridging Table 2 with the following Table 2:

Table 2. Peptide targeting moieties and the organ targeted.

Peptide Sequence	**Organ**
GGG	Bone marrow
GFS	Bone marrow
LWS	Bone marrow
ARL	Bone marrow
FGG	Bone marrow
GVL	Bone marrow
SGT	Bone marrow
EGG	Fat
LLV	Fat
LSP	Fat
EGR	Fat
FGV	Fat
LVS	Muscle
GER	Muscle
AGG	Prostate
EGR	Prostate
GER	Prostate
GVL	Prostate
SMSIARL (SEQ ID NO: 4)	Prostate
GRR	Skin
GGH	Skin
GTV	Skin
ARL	Skin
FGG	Skin
FGV	Skin

SGT	Skin
GVL	Multiple Organs
EGR	Multiple Organs
GFG	Multiple Organs
FGV	Multiple Organs
GFGV (SEQ ID NO: 5)	Multiple Organs
RFGG (SEQ ID NO: 6)	Multiple Organs
FGGS (SEQ ID NO: 7)	Multiple Organs
FGGSV (SEQ ID NO: 8)	Multiple Organs
FGGSW (SEQ ID NO: 9)	Multiple Organs
FGG	Multiple Organs
GERIS (SEQ ID NO: 10)	Multiple Organs
GERLS (SEQ ID NO: 11)	Multiple Organs
GERAG (SEQ ID NO: 12)	Multiple Organs
GER	Multiple Organs
PSGTS (SEQ ID NO: 13)	Multiple Organs
MSGTG (SEQ ID NO: 14)	Multiple Organs
VSGT (SEQ ID NO: 15)	Multiple Organs
LSGT (SEQ ID NO: 16)	Multiple Organs
ISGT (SEQ ID NO: 17)	Multiple Organs
SGT	Multiple Organs
NGR	Atherosclerosis
RGD	Atherosclerosis
CGFECVRQCPERC (SEQ ID NO: 18)	Lung

On page 67 of the specification, please replace the second full paragraph with the following paragraph:

The coupling in the presence of RGD-NH_2 did not produce the expected mono- and/or di-substituted adducts but an unidentified platinum complex with m/z of 690.2. The expected m/z for the mono- and di-substituted are 861.54 and 1188.88, respectively.

On pages 67 and 68 of the specification, please replace the bridging paragraph between these two pages with the following paragraph:

The isotopic pattern as well as the one mass unit difference in between each isotopic line points to a singly charged platinum complex, however, no conclusive chemical structure could be proposed. The non-protected Asp in the RGD-NH_2 peptide may have been activated during

the coupling reaction leading to a non-desirable product. Thus, the protected Fmoc-Asp(ODmab)-OH amino acid was used in the synthesis of the RGD-NH_2 peptide. The Dmab protecting group is cleaved by 2% hydrazine in DMF allowing its specific cleavage while using TFA for the cleavage of the other protecting group. The MALDI-TOF analysis of the obtained product turned out to be that of Fmoc-Asp(ODmab)-OH (m/z (observ.)=666.13, m/z (calc.)=666.7). The calculated m/z for the expected RGD(Odmab)NH_2 peptide is 656.77. It is not clear at this point the cause for the failure of this reaction but the Fmoc on the Asp, which is the first amino acid to be loaded on the resin, was not cleaved thus impeding the elongation of the peptide chain. The RGD-NH_2 coupling approach wasn't pursued any longer but it is important to find a suitable procedure, which allows for the preparation of the RGD-NH_2 peptide containing the Asp side chain protected and for its cleavage under very mild acidic or basic conditions.

On page 68 of the specification, please replace the first full paragraph with the following paragraph:

The reaction in the presence of NGR-NH_2 produced the mono- and di-substituted adducts; the crude mixture was purified by C18-HPLC and peaks with retention times of 15.55 and 15.95 minutes are the two desired compounds (Figure 14).

On page 69 of the specification, please replace the third full paragraph with the following paragraph:

In vitro activity studies of **SUN-M** and **SUN-D** on proliferating endothelial cells was pursued in collaboration with Carmen M. Barnés from the Folkman Group at The Children's Hospital Harvard Medical School. In the first phase of this project we have decided to analyze the compounds activity on Bovine Capillary Endothelial Cells (BCE). The first set of measurements were performed as control experiments, thus cisplatin, *trans*-DDP, complex **2** and complex **2** plus non-conjugated NGR-NH_2 were added at 0.01, 0.1, 1.0, 10 and100 μM to 7,500 BCE cells in the presence of basic fibroblast growth factor (bFGF). The cell number percentage was counted after 72 hours on a Coulter Counter and it was found that the in vitro activity of

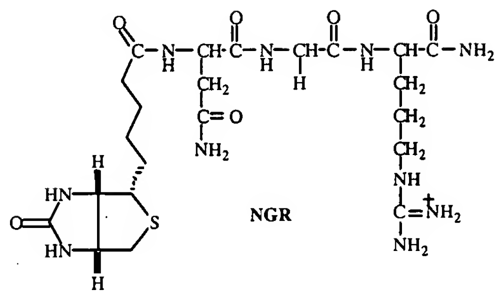
complex **2** and complex **2** plus non-conjugated $NGRNH_2$ are comparable (Figure 18). On the other hand, cisplatin was the most active among the four measured controls. It is important to point out that the percentage of non-induced cells (i.e. normal cells) was 44.8% after 72 hours. Therefore, as concluded from the results that are shown in Figure 18, concentrations above 1.0 μM for cisplatin, 10 μM for *trans*-DDP and 100 μM for complex **2** are toxic also to non-induced proliferating cells.

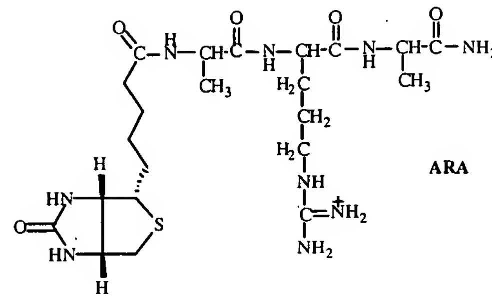
On page 70 of the specification, please replace the fourth full paragraph with the following paragraph:

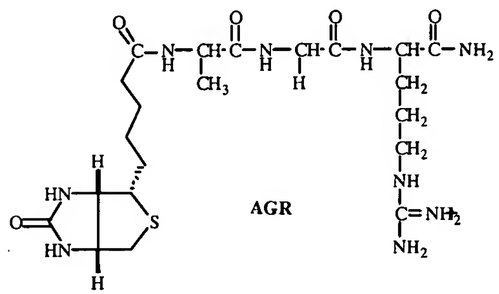
The mixture S1 is more active by 7-10-fold than complex **2** but not as active as cisplatin. The fact that these complexes are more potent than complex **2** is a very promising result and the goal at this point is to show that the selectivity of these compounds is greater than cisplatin. The selectivity of these complexes was investigated by coupling a 'mutated' peptide, AGR-NH_2 to complex **2**. The mono- and di-substituted complex was termed **SAN-M** and **SAN-D**, respectively.

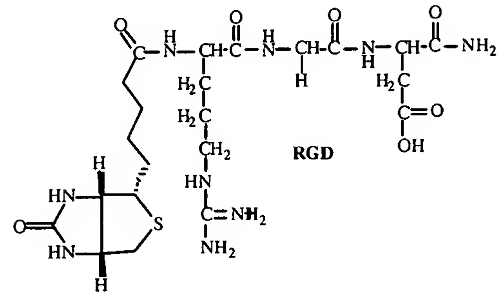
On page 71 of the specification, please replace the third full paragraph with the following paragraph:

Another approach taken to investigate the selectivity of these compounds was by the labeling of NGR-NH_2, RGD-NH_2 and the 'mutated' peptides AGR-NH_2, ARA-NH_2 with biotin. The latter sequence was the one chosen by Ellerby *et al* to show internalization of CNGRC-GG-(pro-apoptotic peptide) (SEQ ID NO: 3) into KS1767 cells derived from Kaposi Sarcoma.









The interaction of biotin with streptavidin-FITC (FITC=fluorescein isothiocyanate) will be used as a probe for internalization. Streptavidin-FITC is known to contain 4-8 moles of (FITC) per mol of streptavidin thus amplifying the fluorescence signal compared to an approach in which only one fluorescein molecule is attached to the peptide. The four biotin labeled compounds were synthesized in the peptide synthesizer and analyzed by LC-MS. The large-scale purification of the labeled peptides is underway.